

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/116,676

DATE: 07/21/98
TIME: 14:20:11

INPUT SET: S27568.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

- 1
- 2
- 3 (1) General Information:
- 4
- 5 (i) APPLICANT: Borowsky, Beth
- 6
- 7 (ii) TITLE OF INVENTION: DNA ENCODING A HUMAN Ob RECEPTOR
- 8 (hOb-Re) AND USES THEREOF
- 9
- 10 (iii) NUMBER OF SEQUENCES: 29
- 11
- 12 (iv) CORRESPONDENCE ADDRESS:
- 13 (A) ADDRESSEE: Cooper & Dunham LLP
- 14 (B) STREET: 1185 Avenue of the Americas
- 15 (C) CITY: New York
- 16 (D) STATE: New York
- 17 (E) COUNTRY: USA
- 18 (F) ZIP: 10036
- 19
- 20 (v) COMPUTER READABLE FORM:
- 21 (A) MEDIUM TYPE: Floppy disk
- 22 (B) COMPUTER: IBM PC compatible
- 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 25
- 26 (vi) CURRENT APPLICATION DATA:
- 27 (A) APPLICATION NUMBER:
- 28 (B) FILING DATE:
- 29 (C) CLASSIFICATION:
- 30
- 31 (viii) ATTORNEY/AGENT INFORMATION:
- 32 (A) NAME: White, John P
- 33 (B) REGISTRATION NUMBER: 28,678
- 34 (C) REFERENCE/DOCKET NUMBER: 1795-53801/JPW/KDB
- 35
- 36 (ix) TELECOMMUNICATION INFORMATION:
- 37 (A) TELEPHONE: 212 278 0400
- 38 (B) TELEFAX: 212 291 0525
- 39
- 40
- 41 (2) INFORMATION FOR SEQ ID NO:1:
- 42
- 43 (i) SEQUENCE CHARACTERISTICS:
- 44 (A) LENGTH: 54 base pairs
- 45 (B) TYPE: nucleic acid
- 46 (C) STRANDEDNESS: single

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47 (D) TOPOLOGY: linear
48
49 (ii) MOLECULE TYPE: DNA
50
51 (ix) FEATURE:
52 (A) NAME/KEY: CDS
53 (B) LOCATION: 1..54
54
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
56
57 AAT GTT AAA AAG TTT CAC ATC CAC GGT ATG TGT ACT GTA CTT TTC ATG 48
58 Asn Val Lys Lys Phe His Ile His Gly Met Cys Thr Val Leu Phe Met
59 1 5 10 15
60
61 GAT TAG 54
62 Asp *
63
64
65
66 (2) INFORMATION FOR SEQ ID NO:2:
67
68 (i) SEQUENCE CHARACTERISTICS:
69 (A) LENGTH: 17 amino acids
70 (B) TYPE: amino acid
71 (D) TOPOLOGY: linear
72
73 (ii) MOLECULE TYPE: protein
74
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
76
77 Asn Val Lys Lys Phe His Ile His Gly Met Cys Thr Val Leu Phe Met
78 1 5 10 15
79
80 Asp
81
82
83
84 (2) INFORMATION FOR SEQ ID NO:3:
85
86 (i) SEQUENCE CHARACTERISTICS:
87 (A) LENGTH: 45 base pairs
88 (B) TYPE: nucleic acid
89 (C) STRANDEDNESS: single
90 (D) TOPOLOGY: linear
91
92 (ii) MOLECULE TYPE: DNA
93
94 (ix) FEATURE:
95 (A) NAME/KEY: CDS
96 (B) LOCATION: 1..45
97
98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
99

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100 TCT GTT AAG AAG TAT TAT ATC CAT GGT AAG TTT ACT ATA CTT TAG 45
101 Ser Val Lys Lys Tyr Tyr Ile His Gly Lys Phe Thr Ile Leu *
102 1 5 10 15
103
104

105 (2) INFORMATION FOR SEQ ID NO:4:

106
107 (i) SEQUENCE CHARACTERISTICS:
108 (A) LENGTH: 14 amino acids
109 (B) TYPE: amino acid
110 (D) TOPOLOGY: linear
111

112 (ii) MOLECULE TYPE: protein

113
114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

115
116 Ser Val Lys Lys Tyr Tyr Ile His Gly Lys Phe Thr Ile Leu
117 1 5 10 15
118
119

120 (2) INFORMATION FOR SEQ ID NO:5:

121
122 (i) SEQUENCE CHARACTERISTICS:
123 (A) LENGTH: 27 base pairs
124 (B) TYPE: nucleic acid
125 (C) STRANDEDNESS: single
126 (D) TOPOLOGY: linear
127

128 (ii) MOLECULE TYPE: DNA

129
130
131 (ix) FEATURE:

132 (A) NAME/KEY: CDS
133 (B) LOCATION: 1..27
134

135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

136
137 GGT ATG TGT ACT GTA CTT TTC ATG GAT 27
138 Gly Met Cys Thr Val Leu Phe Met Asp
139 1 5
140
141

142 (2) INFORMATION FOR SEQ ID NO:6:

143
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 9 amino acids
146 (B) TYPE: amino acid
147 (D) TOPOLOGY: linear
148

149 (ii) MOLECULE TYPE: protein

150
151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

152

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153 Gly Met Cys Thr Val Leu Phe Met Asp
154 1 5
155
156

157 (2) INFORMATION FOR SEQ ID NO:7:
158

159 (i) SEQUENCE CHARACTERISTICS:
160 (A) LENGTH: 18 base pairs
161 (B) TYPE: nucleic acid
162 (C) STRANDEDNESS: single
163 (D) TOPOLOGY: linear
164

165 (ii) MOLECULE TYPE: DNA
166

167 (ix) FEATURE:
168 (A) NAME/KEY: CDS
169 (B) LOCATION: 1..18
170

171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
172

173 GGT AAG TTT ACT ATA CTT
174 Gly Lys Phe Thr Ile Leu
175 10 15
176
177
178

18

179 (2) INFORMATION FOR SEQ ID NO:8:
180

181 (i) SEQUENCE CHARACTERISTICS:
182 (A) LENGTH: 6 amino acids
183 (B) TYPE: amino acid
184 (D) TOPOLOGY: linear
185

186 (ii) MOLECULE TYPE: protein
187188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
189

190 Gly Lys Phe Thr Ile Leu
191 1 5
192
193
194

195 (2) INFORMATION FOR SEQ ID NO:9:
196

197 (i) SEQUENCE CHARACTERISTICS:
198 (A) LENGTH: 2415 base pairs
199 (B) TYPE: nucleic acid
200 (C) STRANDEDNESS: single
201 (D) TOPOLOGY: linear
202

203 (ii) MOLECULE TYPE: DNA
204

205 (ix) FEATURE:

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		(A) NAME/KEY: CDS																		
		(B) LOCATION: 1..2415																		
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:																		
211	ATG	ATT	TGT	CAA	AAA	TTC	TGT	GTG	GTT	TTG	TTA	CAT	TGG	GAA	TTT	ATT	48			
212	Met	Ile	Cys	Gln	Lys	Phe	Cys	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Ile				
213	1				5					10					15					
215	TAT	GTG	ATA	ACT	GCG	TTT	AAC	TTG	TCA	TAT	CCA	ATT	ACT	CCT	TGG	AGA	96			
216	Tyr	Val	Ile	Thr	Ala	Phe	Asn	Leu	Ser	Tyr	Pro	Ile	Thr	Pro	Trp	Arg				
217				20				25					30							
219	TTT	AAG	TTG	TCT	TGC	ATG	CCA	CCA	AAT	TCA	ACC	TAT	GAC	TAC	TTC	CTT	144			
220	Phe	Lys	Leu	Ser	Cys	Met	Pro	Pro	Asn	Ser	Thr	Tyr	Asp	Tyr	Phe	Leu				
221			35					40					45							
223	TTG	CCT	GCT	GGA	CTC	TCA	AAG	AAT	ACT	TCA	AAT	TCG	AAT	GGA	CAT	TAT	192			
224	Leu	Pro	Ala	Gly	Leu	Ser	Lys	Asn	Thr	Ser	Asn	Ser	Asn	Gly	His	Tyr				
225		50					55					60								
227	GAG	ACA	GCT	GTT	GAA	CCT	AAG	TTT	AAT	TCA	AGT	GGT	ACT	CAC	TTT	TCT	240			
228	Glu	Thr	Ala	Val	Glu	Pro	Lys	Phe	Asn	Ser	Ser	Gly	Thr	His	Phe	Ser				
229	65					70					75					80				
231	AAC	TTA	TCC	AAA	ACA	ACT	TTC	CAC	TGT	TGC	TTT	CGG	AGT	GAG	CAA	GAT	288			
232	Asn	Leu	Ser	Lys	Thr	Thr	Phe	His	Cys	Cys	Phe	Arg	Ser	Glu	Gln	Asp				
233				85					90					95						
235	AGA	AAC	TGC	TCC	TTA	TGT	GCA	GAC	AAC	ATT	GAA	GGA	AAG	ACA	TTT	GTT	336			
236	Arg	Asn	Cys	Ser	Leu	Cys	Ala	Asp	Asn	Ile	Glu	Gly	Lys	Thr	Phe	Val				
237				100					105					110						
239	TCA	ACA	GTA	AAT	TCT	TTA	GTT	TTT	CAA	CAA	ATA	GAT	GCA	AAC	TGG	AAC	384			
240	Ser	Thr	Val	Asn	Ser	Leu	Val	Phe	Gln	Gln	Ile	Asp	Ala	Asn	Trp	Asn				
241			115					120					125							
243	ATA	CAG	TGC	TGG	CTA	AAA	GGA	GAC	TTA	AAA	TTA	TTC	ATC	TGT	TAT	GTG	432			
244	Ile	Gln	Cys	Trp	Leu	Lys	Gly	Asp	Leu	Lys	Leu	Phe	Ile	Cys	Tyr	Val				
245		130					135					140								
247	GAG	TCA	TTA	TTT	AAG	AAT	CTA	TTC	AGG	AAT	TAT	AAC	TAT	AAG	GTC	CAT	480			
248	Glu	Ser	Leu	Phe	Lys	Asn	Leu	Phe	Arg	Asn	Tyr	Asn	Tyr	Lys	Val	His				
249	145				150					155					160					
251	CTT	TTA	TAT	GTT	CTG	CCT	GAA													

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
80	Stop Codon at end of sequence removed - no error	
116	Stop Codon at end of sequence removed - no error	
577	Stop Codon at end of sequence removed - no error	